IN THE ABSTRACT

The Abstract as amended below with a replacement Abstract shows added text with underlining and deleted text with ~~strikethrough~~.

Please **REPLACE** the Abstract as marked below to show changes. The replacement Abstract is submitted on a separate sheet (37 CFR 1.72).

--A genetic motif is extracted from at least one piece of input gene arrangement information, and~~,~~ based on the extracted motif, gene arrangement information including~~, as a part thereof,~~ the motif <u>as a part thereof</u> is retrieved from previously ~~clarified~~<u>sequenced</u> gene ~~arrangement~~<u>information</u>. The gene arrangement information as retrieved is added to the input gene arrangement information, to thereby improve a genetic motif extracting efficiency.--

IN THE CLAIMS

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with <u>underlining</u> and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please AMEND claims 2, 8, and 9 in accordance with the following:

1.   (CANCELLED)

2.   (CURRENTLY AMENDED) A genetic motif extracting and processing apparatus comprising:

gene arrangement information storing means for storing gene arrangement information;

gene arrangement information inputting means for inputting at least one piece of gene arrangement information;

motif extraction range designating means for an operator <u>to</u> interactively ~~designating~~<u>designate</u> on a display screen a motif extraction range in the input gene arrangement information;~~and~~

<u>motif extracting means for</u> extracting a genetic motif within the designated extraction range from the input gene arrangement information;

gene arrangement information retrieving means for retrieving, based on the motif extracted from the input gene arrangement information, gene arrangement information including the extracted motif, from said gene arrangement information storing means; and

gene arrangement information adding means for adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information.

3.   (PREVIOUSLY PRESENTED) A genetic motif extracting and processing apparatus according to claim 2, further comprising gene arrangement information editing means for editing the gene arrangement information.

4.   (PREVIOUSLY PRESENTED) A genetic motif extracting and processing apparatus according to claim 2, further comprising motif editing means for editing the motif extracted by the motif extracting means.

5. (PREVIOUSLY PRESENTED) A genetic motif extracting and processing apparatus according to claim 2, further comprising alignment means for alignment-processing a plurality of gene arrangement information input by the gene arrangement information inputting means.

6. (PREVIOUSLY PRESENTED) A genetic motif extracting and processing apparatus according to claim 2, further comprising:

motif storing means for storing motifs; and

motif registering means for registering the motif extracted by the motif extracting means into said motif storing means.

7. (ORIGINAL) A genetic motif extracting and processing apparatus according to claim 6, further comprising motif displaying means for displaying at least one motif from those motifs registered in the motif storing means.

8. (CURRENTLY AMENDED) A genetic motif extracting and processing method comprising:

inputting at least one piece of gene arrangement information for retrieval;

designating interactively on a display screen a motif extraction range in the input gene arrangement information;

extracting a genetic motif within the designated motif extraction range from the input gene arrangement information;

retrieving, based on the motif extracted from the input gene arrangement information, gene arrangement information including the extracted motif, from a gene arrangement information database; and

adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information input for retrieval to repeat the retrieving process of the gene arrangement information.

9.   (CURRENTLY AMENDED) A recording medium recorded with a genetic motif extracting and processing program realizing a process of:

inputting at least one piece of gene arrangement information for retrieval;

designating interactively on a display screen a motif extraction range in the input gene arrangement information;

extracting a genetic motif within the designated motif extraction range from the input gene arrangement information;

retrieving, based on the motif extracted from the input gene arrangement information, gene arrangement information including the extracted motif, from a gene arrangement information database; and

adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information input for retrieval to repeat the retrieving process of the gene arrangement information.

REMARKS

The following remarks and claim amendments are respectfully submitted in response to the Examiner's comments in the Advisory Action and the final Office Action. Because the Advisory Action is not clear regarding entry of the amendments in the After Final Amendment in view of checked items 3 and 7.b, this Amendment provides all amendments to the application, including the previously submitted not entered Abstract replacement, not entered claim amendments as well as additional claim amendments. Reconsideration of the claims in view of the claim amendments, the remarks, and the Examiner interview on October 7, 2003, is respectfully requested.

STATUS OF CLAIMS

Claims 2-9 are pending.

The Abstract is objected to for informalities as indicated by the Examiner.

Claims 2-7 are rejected under 35 USC 112, second paragraph, for indefiniteness.

Claims 8-9 are rejected under 35 USC 103(a) as being unpatentable over Kawanishi (US Patent No. 5,598,350), Attwood (J. Chem. Inf. Comput. Sci. 1997, vol. 3, pp. 417-424), and in view of Marr (US Patent No. 5,701,256). Marr is newly cited, and thus, newly relied upon.

Claims 2, 8 and 9 are amended.

Thus, claims 2-9 remain pending for reconsideration, which is respectfully requested.

No new matter has been asserted in this Amendment. The foregoing rejections are hereby traversed.

IN THE ABSTRACT

The Abstract is replaced with a new Abstract (attached hereto as a separate sheet) taking into consideration the Examiner's comments. Withdrawal of the objection to the Abstract is respectfully requested.

35 USC 112, SECOND PARAGRAPH, REJECTIONS

Claims 2-7 are rejected under 35 USC 112, second paragraph, for indefiniteness. Claim 2 is amended to improve form for overcoming both indefiniteness rejections. In particular, claim 2 is amended to overcome the first and second indefiniteness rejections in view of the interview with the Examiner on October 7, 2003 by reciting, "motif extraction range designating means for

an operator to interactively ~~designating~~designate on a display screen a motif extraction range in the input gene arrangement information; motif extracting means for extracting a genetic motif within the designated extraction range from the input gene arrangement information."

Support for the claim amendments can be found, for example, in page 8, last paragraph, through page 9, 2nd to last paragraph. Withdrawal of the rejections of claims 2-7, and allowance of claims 2-7, because there are no outstanding prior art rejections for independent claim 2, is respectfully requested.

35 USC 103 REJECTIONS

Claims 8-9 are rejected under 35 USC 103(a) as being unpatentable over Kawanishi (US Patent No. 5,598,350), Attwood (J. Chem. Inf. Comput. Sci. 1997, vol. 3, pp. 417-424), and in view of Marr (US Patent No. 5,701,256). Marr is newly cited, and thus, newly relied upon.

As previously asserted in the After Final Amendment of September 23, 2003, and further clarified herein, the patentably distinguishing features of the claimed invention are: (1) to interactively designate the motif extraction range based on gene arrangement information input for retrieval (i.e., as an object to be clarified (sequenced)), (2) to retrieve from a database the gene arrangement information including the motif as a part thereof, and (3) to add the retrieved gene arrangement information to the gene arrangement information input for retrieval. In regard to independent claims 8 and 9, in response to the Examiner's comments in the Advisory Action of October 15, 2003, the Applicants further amend claims 8 and 9 and assert the following:

In regard to claims 8 and 9, the examiner appears to misinterpret "input gene arrangement information" as being stored in a database. However, the input gene arrangement information is merely information to be retrieved, and may be temporarily stored but typically is not stored in any database. Therefore, the Examiner's discussion regarding whether there is one or more databases does not apply to the claimed invention. In other words, the phrase "input gene arrangement information" is used as a term for retrieval, and a retrieval result is linked (added) to this "input gene arrangement information" for repeating the retrieval so that the function and structure of gene arrangement information are gradually presumed (see, pages 5 and 6 of the Application). Accordingly, in view of the Examiner's interpretation, claims 8 and 9 are amended to clarify that "input gene arrangement information is for retrieval" and that the process comprises "adding the retrieved extracted-motif-based gene arrangement information to the ~~input~~ gene arrangement information input for retrieval to repeat the retrieving process of the gene arrangement information."

Therefore, Attwood does not disclose or suggest adding to a gene sequence input for retrieval a gene sequence retrieved from existing gene sequences that includes an interactively extracted motif of the gene sequence input for retrieval. Such adding to the gene sequence input for retrieval based upon the interactive motif extraction has a benefit of reutilizing an interactively designated motif extracted from the gene information input for retrieval (i.e., to be sequenced) by improving a motif extracting efficiency for determining functions and structures of genes. In contrast to the claimed present invention, Attwood adds the new sequence information to the extracted motifs (Attwood, page 418, column 1, 2nd paragraph).

In view of the remarks and the claim amendments, withdrawal of the rejections of claims 8-9 and allowance of claims 8-9 is respectfully requested.
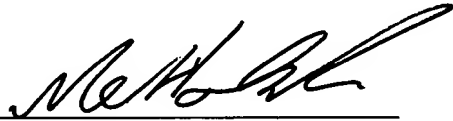
CONCLUSION

Withdrawal of the rejections of claim 2-9 and allowance of claims 2-9 is respectfully requested.

Finally, if there are any formal matters remaining after this response, the Examiner is requested to telephone the undersigned to attend to these matters.

Respectfully submitted,
STAAS & HALSEY LLP

Date: 10/24/2003

By: _____
Mehdi D. Sheikerz
Registration No. 41,307

1201 New York Avenue, NW, Suite 700
Washington, D.C. 20005
Telephone: (202) 434-1500
Facsimile: (202) 434-1501

ABSTRACT

A genetic motif is extracted from at least one piece of input gene arrangement information, and based on the extracted motif, gene arrangement information including the motif as a part thereof is retrieved from previously sequenced gene information. The gene arrangement information as retrieved is added to the input gene arrangement information, to thereby improve a genetic motif extracting efficiency.